

SEQUENCE LISTING

<110> Liao and Zeldin

<120> ANTI-INFLAMMATORY ACTIONS OF CYTOCHROME P450 EPOXYGENASE-DERIVED
EICOSANOIDS

<130> 4239-62631/WDN/SLR

<140> US 09/634,369

<141> 2000-08-09

<150> US 60/148,434

<151> 1999-08-11

<160> 4

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

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tgg cgc ttg ccc ttc ctt ggc aac ttc ttc ctt gtg gac ttc gag cag	96
Trp Arg Leu Pro Phe Leu Gly Asn Phe Phe Leu Val Asp Phe Glu Gln	
20 25 30	

tcg cac ctg gag gtt cag ctg ttt gtg aag aaa tat ggg aac ctt ttt	144
Ser His Leu Glu Val Gln Leu Phe Val Lys Lys Tyr Gly Asn Leu Phe	
35 40 45	

agc ttg gag ctt ggt gac ata tct gca gtt ctt att act ggc ttg ccc	192
Ser Leu Glu Leu Gly Asp Ile Ser Ala Val Leu Ile Thr Gly Leu Pro	
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tta atc aaa gaa gcc ctt atc cac atg gac caa aac ttt ggg aac cgc	240
Leu Ile Lys Glu Ala Leu Ile His Met Asp Gln Asn Phe Gly Asn Arg	
65 70 75 80	

ccc gtg acc cct atg cga gaa cat atc ttt aag aaa aat gga ttg att	288
Pro Val Thr Pro Met Arg Glu His Ile Phe Lys Lys Asn Gly Leu Ile	
85 90 95	

atg tca agt ggc cag gca tgg aag gag caa aga agg ttc act ctg aca	336
Met Ser Ser Gly Gln Ala Trp Lys Glu Gln Arg Arg Phe Thr Leu Thr	
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03 APR 28 AM 9:56

gca cta agg aac ttt ggt tta gga aag aag ggc tta gag gaa cgc att Ala Leu Arg Asn Phe Gly Leu Gly Lys Lys Gly Leu Glu Glu Arg Ile 115 120 125	384
cag gag gag gcc caa cac ctc act gaa gca ata aaa gag gag aac gga Gln Glu Glu Ala Gln His Leu Thr Glu Ala Ile Lys Glu Glu Asn Gly 130 135 140	432
cag cct ttt gac cct cat ttc aag atc aac aat gca gtt tcc aat atc Gln Pro Phe Asp Pro His Phe Lys Ile Asn Asn Ala Val Ser Asn Ile 145 150 155 160	480
att tgc tcc atc acc ttc gga gaa cgc ttt gag tac cag gat agt tgg Ile Cys Ser Ile Thr Phe Gly Glu Arg Phe Glu Tyr Gln Asp Ser Trp 165 170 175	528
ttt cag cag ctg ctg aag tta cta gat gaa gtc aca tac ttg gag gct Phe Gln Gln Leu Leu Lys Leu Leu Asp Glu Val Thr Tyr Leu Glu Ala 180 185 190	576
tca aag aca tgc cag ctc tac aat gtc ttt cca tgg ata atg aaa ttc Ser Lys Thr Cys Gln Leu Tyr Asn Val Phe Pro Trp Ile Met Lys Phe 195 200 205	624
ctg cct gga ccc cac caa act ctc ttc agc aac tgg aaa aaa ctg aaa Leu Pro Gly Pro His Gln Thr Leu Phe Ser Asn Trp Lys Lys Leu Lys 210 215 220	672
ttg ttt gtt tct cat atg att gac aaa cac aga aag gat tgg aat cct Leu Phe Val Ser His Met Ile Asp Lys His Arg Lys Asp Trp Asn Pro 225 230 235 240	720
gca gaa aca aga gac ttt att gat gct tac ctt aaa gaa atg tca aag Ala Glu Thr Arg Asp Phe Ile Asp Ala Tyr Leu Lys Glu Met Ser Lys 245 250 255	768
cac aca ggc aat cct act tca agt ttc cat gaa gaa aac ctc atc tgc His Thr Gly Asn Pro Thr Ser Ser Phe His Glu Glu Asn Leu Ile Cys 260 265 270	816
agc acc ctg gac ctc ttc ttt gcc gga acc gag aca act tcc aca act Ser Thr Leu Asp Leu Phe Phe Ala Gly Thr Glu Thr Thr Ser Thr Thr 275 280 285	864
ctg cga tgg gct ctg ctt tat atg gcc ctc tac cca gaa atc caa gaa Leu Arg Trp Ala Leu Leu Tyr Met Ala Leu Tyr Pro Glu Ile Gln Glu 290 295 300	912
aaa gta caa gtc gag att gac aga gtg att ggc cag ggg cag cag ccg Lys Val Gln Val Glu Ile Asp Arg Val Ile Gly Gln Gly Gln Gln Pro 305 310 315 320	960
agc aca gcc gcc cgg gag tcc atg ccc tac acc aat gct gtc atc cat Ser Thr Ala Ala Arg Glu Ser Met Pro Tyr Thr Asn Ala Val Ile His 325 330 335	1008

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Ser His Leu Glu Val Gln Leu Phe Val Lys Lys Tyr Gly Asn Leu Phe
 35 40 45

Ser Leu Glu Leu Gly Asp Ile Ser Ala Val Leu Ile Thr Gly Leu Pro
 50 55 60

Leu Ile Lys Glu Ala Leu Ile His Met Asp Gln Asn Phe Gly Asn Arg
 65 70 75 80

Pro Val Thr Pro Met Arg Glu His Ile Phe Lys Lys Asn Gly Leu Ile
 85 90 95

Met Ser Ser Gly Gln Ala Trp Lys Glu Gln Arg Arg Phe Thr Leu Thr
 100 105 110

Ala Leu Arg Asn Phe Gly Leu Gly Lys Lys Gly Leu Glu Glu Arg Ile
 115 120 125

Gln Glu Glu Ala Gln His Leu Thr Glu Ala Ile Lys Glu Glu Asn Gly
 130 135 140

Gln Pro Phe Asp Pro His Phe Lys Ile Asn Asn Ala Val Ser Asn Ile
 145 150 155 160

Ile Cys Ser Ile Thr Phe Gly Glu Arg Phe Glu Tyr Gln Asp Ser Trp
 165 170 175

Phe Gln Gln Leu Leu Lys Leu Leu Asp Glu Val Thr Tyr Leu Glu Ala

180	185	190
Ser Lys Thr Cys Gln Leu Tyr Asn Val Phe Pro Trp Ile Met Lys Phe		
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Leu Pro Gly Pro His Gln Thr Leu Phe Ser Asn Trp Lys Lys Leu Lys		
210	215	220
Leu Phe Val Ser His Met Ile Asp Lys His Arg Lys Asp Trp Asn Pro		
225	230	235
Ala Glu Thr Arg Asp Phe Ile Asp Ala Tyr Leu Lys Glu Met Ser Lys		
245	250	255
His Thr Gly Asn Pro Thr Ser Ser Phe His Glu Glu Asn Leu Ile Cys		
260	265	270
Ser Thr Leu Asp Leu Phe Phe Ala Gly Thr Glu Thr Thr Ser Thr Thr		
275	280	285
Leu Arg Trp Ala Leu Leu Tyr Met Ala Leu Tyr Pro Glu Ile Gln Glu		
290	295	300
Lys Val Gln Val Glu Ile Asp Arg Val Ile Gly Gln Gly Gln Gln Pro		
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